Effects of sire line, sire, and sex on plasma urea nitrogen, body weight, and backfat thickness in offspring of Duroc and Landrace boars[1,2]

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ABSTRACT: In pork production, the efficiency of dietary protein (AA) use is low, resulting in urinary excretion of large quantities of nitrogen as urea. Use of AA and formation of urea are under enzymatic regulation, suggesting genetic regulation. The current study examined the effects of sire line, sire, and sex on growth characteristics and plasma urea nitrogen (PUN) concentrations in the offspring of 11 Duroc sires and 11 Landrace sires bred to Yorkshire-Landrace dams. Plasma samples were obtained at approximately 107 (age class = 107 d), 128 (age class = 128 d), and 149 (age class = 149 d) d of age from 511 boars, gilts, and barrows group-penned and fed standard finishing diets. Body weight and backfat (BF, mean of 3 measurements) were recorded at the time of blood sample collection. Sex, age class, and their interaction influenced ($P < 0.01$) BW, BF, and PUN. Predicted traits (i.e., ADG, BW at 21 wk, average daily change in BF, BF at 21 wk, and the mean of 3 PUN measures) were generated. Means (±SD) were: ADG, 888 ± 204 g; BW at 21 wk, 94.2 ± 12.5 kg; average daily change in BF, 0.083 ± 0.052 mm; BF at 21 wk, 13.8 ± 3.0 mm; and the mean of 3 PUN measures, 16.2 ± 4.4 mg/dL. Predicted weight traits were influenced ($P < 0.05$) by sire line, and sex influenced ($P < 0.01$) all predicted traits. Heritability estimates for PUN at 107, 128, and 149 d of age were 0.35 ± 0.15, 0.21 ± 0.13, and 0.16 ± 0.12, respectively. Phenotypic correlations of PUN with growth and fat traits were low. Genetic correlations of PUN measured at 107 d with growth and fat traits were low. However, genetic correlations of PUN measured at 128 or 149 d with growth and fat traits ranged from 0.81 to 0.95. Determination of PUN, as herein, may be of sufficient precision to allow its use in a selection protocol. Selection of pigs with superior growth performance and low PUN may result in a greater efficiency of dietary nitrogen use and a reduced negative environmental impact.

Key words: genetic influence, growth, plasma urea nitrogen

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INTRODUCTION

Among the problems facing the swine industry are inefficient use of inputs, particularly dietary AA, which account for approximately 25% of feed costs, and management and disposal of manure. Contributing to inefficiency of AA use are dietary recommendations for AA that have been developed for populations and diets that are formulated to ensure only a few individuals are fed below their individual requirements. Amino acids fed in excess of requirements for tissue repair and accretion are transaminated or deaminated or both, and the nitrogen moiety is converted to urea in the liver (Salway, 1994). Urea is excreted in urine. Urinary excretion and circulating concentrations of urea have been measured in evaluation of AA requirements of swine under different physiological conditions. Coma et al. (1995) used plasma urea nitrogen concentrations (**PUN**) to monitor dietary AA adequacy in growing gilts and found PUN values have potential as an indicator of efficiency of lean tissue growth. Additionally, the response in PUN to diet is influenced by initial PUN, that is, PUN while pigs were fed a common diet, indicating individuality in PUN and possibly a genetic influence. Chen et al. (1999) determined optimal dietary concentrations of CP, source of AA, as evaluated by rate and efficiency of BW gain. In addition, PUN was positively correlated with dietary CP. Feeding CP or AA in excess results in high PUN, which is excreted in the urine and subsequently converted to ammonia, a volatile environmental pollutant. Thus, problems of manure management are inextricably associated with inefficient use of dietary nitrogen.

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Table 1. Distribution within sires and sexes of pigs sampled

Sire	Sire line	No. of pigs	No. of litters	No. of boars	No. of gilts	No. of barrows
22	Duroc	24	6	6	9	9
56	Duroc	25	7	6	9	10
63	Duroc	22	7	6	6	10
67	Duroc	26	7	6	10	10
98	Duroc	21	6	5	7	9
99	Duroc	20	6	5	8	7
143	Duroc	23	6	5	8	10
871	Duroc	25	6	6	9	10
973	Duroc	24	7	6	8	10
989	Duroc	22	7	6	6	10
2411	Duroc	26	5	6	10	10
16	Landrace	24	6	6	8	10
81	Landrace	25	7	6	9	10
90	Landrace	27	4	7	12	8
172	Landrace	23	6	5	8	10
232	Landrace	21	5	6	5	10
341	Landrace	20	5	6	6	8
402	Landrace	24	5	6	8	10
673	Landrace	24	6	6	8	10
2650	Landrace	24	6	5	9	10
5201	Landrace	24	7	6	8	10
7201	Landrace	17	6	6	2	9
All		511	133	128	173	210

The objective was to evaluate the relationship between PUN and performance traits and the effect of sire line or breed and sex. An additional objective was to determine the influence of additive genetic variation on PUN and performance traits and ultimately evaluate the potential efficacy of PUN as a quantitative trait.

MATERIALS AND METHODS

All animal procedures were reviewed and approved by the US Meat Animal Research Center Animal Care and Use Committee.

Animals used were from initial crosses in production of a swine resource population developed to provide for identification of QTL for production traits. Dams were a broad sample from a Yorkshire × maternal Landrace composite population. Sires were 11 unrelated Duroc boars and 11 unrelated high-lean terminal Landrace boars obtained from commercial AI companies. Boars used were selected to be representative of the breeds.

Boars, barrows, and gilts (n = 511) from 2 farrowing groups were selected for sampling for the current study. Average birth dates were May 14 (SD = 6.7) and July 17 (SD = 5.9). Distribution of pigs within sires and sexes is presented in Table 1. Throughout the study, pigs were housed in group pens in an enclosed growing/finishing facility, segregated by sex (10 to 15 pigs per pen, depending on size of the pen; minimum of 0.95 m^2 allocated for each pig). Feed consisted of ground corn-soybean meal, 3-phase, growing-finishing diets that met or exceeded recommendations (NRC, 1998) and was provided ad libitum in self-feeders. Diet composition and the 3-phase growing-finishing regimen are presented in Table 2.

Blood was sampled from randomly chosen healthy gilts and barrows and all available intact males. Blood samples were collected at approximately 107 (102 to 110; age class = 107 d), 128 (123 to 131; age class = 128 d), and 149 (144 to 152; age class = 149 d) d of age. These 3 ages were chosen for blood sample collection and recording of BW and backfat thickness because they were predicted to span the portion of the growing-finishing period when most of the feed is consumed, approximately 50 kg of BW to near slaughter weight, and provide a reasonable estimate of PUN and rates of BW and backfat gain over that period. At each sampling, blood samples were collected into 10-mL heparinized syringes via jugular venipuncture and immediately placed in ice. Within 4 h of collection, plasma was aspirated and frozen for subsequent laboratory analysis of urea nitrogen.

Plasma samples were analyzed for urea nitrogen using a Technicon Autoanalyzer (Marsh et al., 1965). On the day of or the day after blood sample collection, BW and average backfat thickness (**AvBF**) were recorded. Backfat was measured ultrasonically (Lean-Meater, Renco Corp., Minneapolis, MN) 5 to 8 cm lateral to the midline at the first rib, last rib, and last lumbar vertebrae, and these 3 measures were averaged to obtain AvBF. Average daily gain and average daily change in backfat thickness (**ADCBF**), which are accretive measures and were estimated while the animals were in the finishing facility, were determined by within-pig linear regression using the 3 recorded BW and AvBF

Table 2. Feed fed during the course of the study

Ingredient, % as fed	Grower #1 8 to 13 wk[1]	Grower #2 13 to 16 wk[1]	Finisher 16 wk to end[1]
Ground corn	70.65	76.28	79.08
Soybean meal, 44% CP	25.01	20.02	17.55
Dicalcium phosphate	1.17	0.76	0.61
Ground limestone	0.96	0.84	0.82
Sodium chloride	0.30	0.30	0.30
Vitamin premix[2]	0.20	0.20	0.20
Trace mineral[3]	0.20	0.20	0.20
Choline chloride	0.10	0.10	0.10
L-Lys	0.24	0.17	0.12
Met	0.01	—	—
Thr	0.06	0.02	0.01
Chlortetracycline 50	0.10	0.10	—
BMD[4]	—	—	0.03
Soybean oil	1.00	1.00	1.00
Total	100.00	100.00	100.00
Calculated nutrient composition, DM basis			
ME, kcal/kg	3,353	3,377	3,388
CP, %	18.00	16.00	15.00
Calcium, %	0.75	0.60	0.55
Phosphorus, %	0.59	0.49	0.46
Lys, %	1.18	0.97	0.86

[1]Age range over which the diet was fed.
[2]Vitamin A (retinyl acetate), 2,200,000 IU/kg; vitamin D_3 (cholecalciferol), 440,000 IU/kg; vitamin E (DL-α-tocopheryl acetate), 17,600 IU/kg; vitamin K (menadione sodium bisulfite complex), 2,200 mg/kg; niacin, 22,000 mg/kg; D-pantothenic acid (D-calcium-pantothenate), 12,100 mg/kg; riboflavin, 4,400 mg/kg; and vitamin B_{12}, 22 mg/kg.
[3]Ferrous sulfate heptahydrate, 35.05%; copper sulfate pentahydrate, 1.77%; manganese oxide, 9.62%; calcium iodate, 0.016%; sodium selenite, 0.033%; and calcium carbonate, 50.91%.
[4]Bacitracin methylene disalicylate.

measures. Parameters of the linear regression equations were used to predict BW (**BW21wk**) and AvBF (**BF21wk**) at 21 wk of age for each pig. The 3 determinations of PUN, a circulating moiety, were averaged to obtain average or mean plasma urea nitrogen (**mPUN**).

Temporal and predicted performance variables and PUN data were examined utilizing the Mixed model procedures of SAS (SAS Inst. Inc., Cary, NC). Mixed model analyses of temporal data are presented in Table 3. The model used for temporal traits included sire line, sex, age class, and all interactions among them, and farrowing season nested within age class, as fixed effects. Sire and litter, both nested within age class, were included as random effects. Mixed model analyses of predicted traits are presented in Table 4. The model for predicted traits was the same as for temporal traits, except age class and its interactions were not included, and no effects were nested within age class. The Kenward-Roger method was used to compute the denominator df.

Table 3. Mixed-model analyses of variance of traits measured over age class[1]

Source	NDF[2]	DDF[3]	BW, kg	AvBF,[4] mm	PUN,[5] mg/dL
Sire line	1	19.6 to 21.2	0.01[6]	0.16	0.06
Sex	2	425 to 458	0.01	0.01	0.01
Line × sex	2	462 to 468	0.16	0.68	0.25
Age class[7]	2	216 to 289	0.01	0.01	0.02
Line × age class	2	19.6 to 26.7	0.16	0.83	0.57
Sex × age class	4	518 to 562	0.01	0.01	0.01
Line × sex × age class	4	549 to 566	0.06	0.04	0.11
Farrowing season (age class)	3	217 to 280	0.01	0.01	0.01

[1]Random sources of variation: sire(age class) and litter(age class).
[2]Numerator df.
[3]Denominator df. The denominator df differ slightly for each trait with the Kenward-Roger method of determination. The range over the 3 traits is presented.
[4]Average backfat thickness measures at first rib, last rib, and last lumbar vertebra.
[5]Plasma urea nitrogen concentration.
[6]Probability of a Type I error.
[7]Age classes are: 107 d, 102 to 110 d of age; 128 d, 123 to 131 d of age; and 149 d, 144 to 152 d of age.

Table 4. Mixed-model analyses of variance of predicted traits[1]

Source	NDF[2]	DDF[3]	ADG,[4] kg/d	BW21wk,[5] kg	ADCBF,[6] mm/d	BF21wk,[7] mm	mPUN,[8] mg/dL
Line	1	20.2 to 21.1	0.05[9]	0.01	0.70	0.23	0.07
Sex	2	425 to 464	0.01	0.01	0.01	0.01	0.01
Line × sex	2	462 to 466	0.66	0.16	0.28	0.31	0.28
Farrowing group	42	211 to 263	0.01	0.01	0.17	0.09	0.01

[1]Random sources of variation: Sire and litter.
[2]Numerator df.
[3]Denominator df. The DDF differ slightly for each trait with the Kenward-Roger method of determination. The range over the 5 traits is presented.
[4]ADG = average daily BW gain from approximately 107 to 149 d of age.
[5]BW21wk = predicted BW at 21 wk of age.
[6]ADCBF = average daily change in average backfat thickness from approximately 107 to 149 d of age.
[7]BF21wk = predicted average backfat thickness at 21 wk of age.
[8]mPUN = mean of plasma urea nitrogen measured at approximately 107, 128, and 149 d of age.
[9]Probability of Type I error.

Heritabilities and phenotypic and genetic correlations were obtained using the derivative-free REML procedure implemented in the software, MTDFREML (Boldman et al., 1995), treating PUN at 107 d (**PUN107**), 128 d (**PUN128**), and 149 d (**PUN149**) as separate traits. The multiple-trait animal model included 7 traits: PUN107, PUN128, PUN149, ADG, BW21wk, ADCBF, and BF21wk, and included sire line, sex, and farrowing season as fixed effects. Litter and polygenic effects were fit as random, with sires and dams assumed unrelated. Single-trait analyses were conducted to obtain beginning values for variance components in a series of 4-trait analyses that provided estimates of all correlations. The 4-trait analyses converged rapidly. The estimates from the 4-trait analyses were averaged, adjusted to achieve positive definiteness, and used as beginning values in the 7-trait analysis. The 7-trait analysis converged slowly. All results reported are from the 7-trait analysis.

RESULTS

Farrowing season, sex, and interaction of sex and age class influenced ($P < 0.01$) BW, AvBF, and PUN (Table 3). Least-squares means for the main effects significant ($P < 0.05$) in the analyses are presented in Table 5. Body weights were greatest in boars and barrows and least in gilts. Average backfat was greatest in barrows and least in boars. Plasma urea nitrogen concentrations were greatest in barrows or gilts (depending on age) and least in boars. Pigs sired by Duroc boars had greater BW. All temporal measures increased with age class.

Temporal measures were used to predict mPUN, ADG, ADCBF, wt21wk, and BF21wk. Results of ANOVA of the predicted traits are presented in Table 4. Only sex affected all predicted traits. Sire line and farrowing season affected ADG and BW21wk, and farrowing season also affected mPUN.

The estimated heritability of PUN (Table 6) varied considerably by age class, decreasing from 0.35 at 107 d to 0.16 at 149 d. However, the litter variance, as a proportion of phenotypic variance (Table 7), increased from 0.09 at 107 d to 0.16 at 149 d. This may be due to sampling error in partitioning of variance between the additive genetic and litter components of variance. The total proportion of variance that accounted for additive genetic and litter effects decreased with age but less dramatically than heritability.

Although PUN was greatest in heritability at 107 d of age, the genetic correlations of PUN107 with PUN128, PUN149, ADG, BW21wk, ADCBF, and BF21wk were all low. To the contrary, the genetic correlation between PUN128 and PUN149 was 0.92, and the genetic correlations of these 2 measures of PUN with ADG, BW21wk, ADCBF, and BF21wk were all high, ranging from 0.87 to 0.95 for PUN128 and from 0.81 to 0.85 for PUN149. These correlations suggest that PUN measured at different times in the finishing period should not be considered the same trait, genetically.

Environmental (Table 6) and phenotypic (Table 7) correlations among PUN traits or among growth and backfat traits were generally moderate in magnitude and positive in direction. However, environmental and phenotypic correlations between these 2 groups of traits were generally of low magnitude. Correlations among litter effects (Table 7) tended to follow the same general pattern but were somewhat erratic and had much greater SE.

DISCUSSION

In this group of pigs, sire within line and interaction of sex and age class influenced temporal measurements of BW, AvBF, and PUN. The influence of sire within line on BW and AvBF was expected. Body weight and AvBF are known to be genetically determined quantitative or additive traits and have been capitalized by quantitative methods. A primary question in this study was whether PUN is genetically determined and whether it may be an exploitable quantitative trait. The heritability estimates for PUN ranged from 0.16 to 0.35, and thus PUN appears to be a candidate for exploitation as a quantitative trait.

Table 5. Body weight, backfat thickness, and plasma urea nitrogen concentrations in the line and sex groups over age class[1]

Trait	Age class[2]		
Effect	107 d	128 d	149 d
Body weight, kg			
Sire line × age class			
Duroc	60.4 ± 0.7	79.0 ± 1.0	99.0 ± 1.4
Landrace	57.6 ± 0.7	74.6 ± 1.0	93.3 ± 1.4
Sex × age class			
Boar	59.2 ± 0.7	78.7 ± 1.0	98.5 ± 1.3
Gilt	58.5 ± 0.6	74.8 ± 0.9	92.5 ± 1.2
Barrow	59.3 ± 0.6	77.0 ± 0.9	97.5 ± 1.2
Average backfat thickness, mm			
Sex × age class			
Boar	9.67 ± 0.20	11.28 ± 0.26	12.39 ± 0.36
Gilt	10.26 ± 0.18	11.52 ± 0.25	13.05 ± 0.34
Barrow	11.18 ± 0.18	12.91 ± 0.25	15.62 ± 0.34
Plasma urea nitrogen, mg/dL			
Sex × age class			
Boar	13.02 ± 0.56	12.72 ± 0.48	15.16 ± 0.45
Gilt	16.19 ± 0.52	16.63 ± 0.44	17.35 ± 0.40
Barrow	15.62 ± 0.52	16.41 ± 0.44	20.08 ± 0.40

[1]Least-squares means from the Mixed model ANOVA presented in Table 3. Only least-squares means for main effects that were significant ($P \leq 0.05$) are presented.
[2]Age classes are: 107 d, 102 to 110 d of age; 128 d, 123 to 131 d of age; and 149 d, 144 to 152 d of age.

The premise of this work is that PUN may be an easily measured index or phenotypic marker of efficiency of AA use for maintenance and accretion of lean tissue applicable in selection programs. Plasma urea nitrogen concentrations, as well as urinary excretion of urea, have been measured to estimate AA requirements (Brown and Cline, 1974; Coma et al., 1995; Chen et al., 1995). In normal, healthy animals, circulating urea concentrations are primarily determined by ammonia availability resulting from transamination and deamination of AA and hepatic production of urea via the Kerbs-Henseleit ornithine or urea cycle in the liver (Salway, 1994). The availability of ammonia for urea synthesis in animals such as growing-finishing pigs is determined by the AA content of the diet relative to AA requirements for protein accretion. If AA are consumed in excess, relative to potential for protein accretion or dietary energy, or in unbalanced proportions, the AA that cannot be used in protein synthesis undergo transamination and deamination. In the Krebs-Henseleit ornithine or urea cycle, the amino moiety is removed and converted to ammonia, and the carbon skeleton is ultimately used for energy or synthesis of nonnitrogenous substances such as glucose, glycogen, or fatty acids. The ammonia, which is toxic, is converted to urea, primarily in the liver, and ultimately excreted via the

Table 6. Heritabilities and genetic and environmental correlations among predicted traits[1]

	PUN107[2]	PUN128[3]	PUN149[4]	ADG[5]	BW21wk[6]	ADCBF[7]	BF21wk[8]
PUN107	**0.35** ± 0.15[9]	0.52 ± 0.09[10]	0.27 ± 0.09	0.00 ± 0.14	0.01 ± 0.14	0.24 ± 0.12	0.38 ± 0.13
PUN128	0.13 ± 0.38[11]	**0.21** ± 0.13	0.34 ± 0.08	–0.32 ± 0.17	–0.13 ± 0.15	0.00 ± 0.12	0.12 ± 0.13
PUN149	0.27 ± 0.39	0.92 ± 0.21	**0.16** ± 0.12	–0.03 ± 0.13	0.03 ± 0.12	0.05 ± 0.11	0.15 ± 0.12
ADG	–0.09 ± 0.29	0.95 ± 0.30	0.81 ± 0.35	**0.52** ± 0.16	0.74 ± 0.07	0.55 ± 0.09	0.38 ± 0.14
BW21wk	0.28 ± 0.32	0.94 ± 0.34	0.85 ± 0.42	0.90 ± 0.08	**0.39** ± 0.18	0.45 ± 0.11	0.65 ± 0.10
ADCBF	0.00 ± 0.30	0.89 ± 0.27	0.82 ± 0.32	0.80 ± 0.11	0.74 ± 0.19	**0.41** ± 0.14	0.67 ± 0.07
BF21wk	0.23 ± 0.27	0.87 ± 0.23	0.84 ± 0.28	0.74 ± 0.12	0.72 ± 0.15	0.96 ± 0.06	**0.55** ± 0.16

[1]Estimates obtained using a multiple-trait REML procedure.
[2]PUN107 = plasma urea nitrogen (PUN) measured at approximately 107 d of age.
[3]PUN128 = PUN measured at approximately 128 d of age.
[4]PUN149 = PUN measured at approximately 149 d of age.
[5]ADG = average daily BW gain from approximately 107 to 149 d of age.
[6]BW21wk = predicted BW at 21 wk of age.
[7]ADCBF = average daily change in average backfat thickness from approximately 107 to 149 d of age.
[8]BF21wk = predicted average backfat thickness at 21 wk of age.
[9]Heritabilities are on the diagonal, which is indicated with bold text.
[10]Phenotypic correlations are above the diagonal, which is indicated with bold text.
[11]Genetic correlations are below the diagonal, which is indicated with bold text.

Table 7. Litter and phenotypic correlations among predicted traits[1]

Env	PUN107[2]	PUN128[3]	PUN149[4]	ADG[5]	BW21wk[6]	ADCBF[7]	BF21wk[8]
PUN107	**0.09** ± 0.07[9]	0.43[10]	0.34	–0.06	0.12	0.13	0.31
PUN128	0.72 ± 0.29[11]	**0.18** ± 0.07	0.53	0.10	0.20	0.25	0.38
PUN149	0.93 ± 0.31	0.81 ± 0.15	**0.16** ± 0.07	0.16	0.21	0.24	0.35
ADG	–0.35 ± 0.70	–0.48 ± 0.62	–0.54 ± 0.68	**0.05** ± 0.06	0.80	0.65	0.57
BW21wk	0.11 ± 0.43	0.00 ± 0.32	–0.13 ± 0.35	0.82 ± 0.20	**0.15** ± 0.08	0.54	0.67
ADCBF	–0.17 ± 0.90	–0.09 ± 0.68	–0.06 ± 0.70	0.47 ± 0.76	0.23 ± 0.62	**0.03** ± 0.06	0.77
BF21wk	0.46 ± 0.93	0.31 ± 0.66	0.20 ± 0.73	0.34 ± 1.07	0.75 ± 0.62	–0.33 ± 0.71	**0.02** ± 0.06

[1]Estimates obtained using a multiple-trait REML procedure.
[2]PUN107 = plasma urea nitrogen (PUN) measured at approximately 107 d of age.
[3]PUN128 = PUN measured at approximately 128 d of age.
[4]PUN149 = PUN measured at approximately 149 d of age.
[5]ADG = average daily BW gain from approximately 107 to 149 d of age.
[6]BW21wk = predicted BW at 21 wk of age.
[7]ADCBF = average daily change in average backfat thickness from approximately 107 to 149 d of age.
[8]BF21wk = predicted average backfat thickness at 21 wk of age.
[9]Litter variance is as a proportion of phenotypic variance on the diagonal, which is indicated with bold text.
[10]Phenotypic correlations are above the diagonal, which is indicated with bold text.
[11]Litter effect correlations are below the diagonal, which is indicated with bold text.

kidneys. Feeding a diet high in CP results in greater activity of hepatic urea cycle enzymes (Rosebrough et al., 1983), and increasing AA requirement for protein synthesis decreases the activity of those enzymes (Bush et al., 2002). In contemporary swine production systems, diets are formulated to achieve the optimal balance of AA based on the best knowledge of AA requirements of growing-finishing pigs within economic constraints imposed by feed ingredient prices (NRC, 1998). Consequently, the most probable cause of high PUN in swine is consumption of a diet that provides AA in excess of the requirement to meet the potential for protein accretion. An individual may consume excess AA because the AA content of the diet is in excess of that individual's AA requirements, the AA content of the diet is improperly formulated for that individual, or that individual may consume excess quantities of the diet through hyperphagia (overconsumption of both energy and AA).

Efficiency of dietary nitrogen retention is low in pigs; very little of the consumed AA are incorporated into body protein. Analysis of data presented by Reeds et al. (1980) indicated that over a growing-finishing period of 30 to 97 kg, 23% of the ingested nitrogen is retained. A portion of this inefficiency is due to indigestibility of AA. True ileal digestibilities of essential AA range from 78 to 93% (NRC, 1998). This is the proportion of ingested AA that have disappeared when the digesta reaches the terminal ileum. Amino acids disappear from the gastrointestinal tract due to metabolism within the gastrointestinal tract or absorption through the wall of the small intestine and entry into the circulation. Amino acids that enter the circulatory system of the pig can be incorporated into body tissue, enzymes, protein hormones, and other regulatory moieties. Amino acids that are not incorporated into proteins are catabolized, and the amino groups are ultimately incorporated into urea. The circulating quantities of this urea, arising from digested and absorbed AA that are not used for synthesis of body proteins, was measured as PUN herein and is primarily excreted in the urine.

An objective of pork production is efficient production of marketable lean product. Protein is a major component of marketable lean product. Rate and efficiency of protein accretion are determinants of rate and efficiency of marketable lean product accretion (Leymaster and Jenkins, 1985). In pork production, accretion of lean product can be approximated from live BW gains, particularly if a measure of fatness (e.g., ultrasonically measured backfat thickness) is included. Estimates of marketable product can be obtained from trimmed lean cuts in pigs. Actual measurement of lean or protein accretion is much more difficult. Measurement of whole body protein accretion requires slaughter of the animal as does acquisition of trimmed lean cuts data. As for the components of protein accretion, measurements of protein synthesis and degradation are expensive and difficult. Efficiency of dietary nitrogen retention (nitrogen balance) can be measured; however, it is labor intensive. Ideally, efficiency of dietary AA use for accretion of body proteins would be estimated from measurement of AA intake, or better AA absorption from the small intestine, and measurement of protein accretion.

Quantification of protein accretion, synthesis, and degradation, and nitrogen balance cannot be accomplished within the physical and fiscal limitations of most research laboratories on a sufficient number of individuals to be of use in determination of genetic parameters. Herein, we estimated genetic parameters for the traits measured, including mPUN, using data from 511 individuals. Estimates of the heritability of PUN ranged from 0.16 to 0.35, indicating it may be an exploitable quantitative trait that has potential in the identification of animals with superior efficiency of AA use for accretion of marketable product.

Herein, we report genotype and sex influences on PUN in swine. There are environmental influences on

PUN in swine, particularly nitrogen intake (Chen et al., 1995). In pigs that are growing, the relationship between dietary nitrogen intake and PUN is positive, even in young pigs fed a diet extremely low in dietary protein (Pond et al., 1992). Time in relation to meal consumption influences PUN and urea excretion (Reeds and Fuller, 1983; Cai et al., 1994; Whang and Easter, 2000). Ideally, blood samples for measurement of PUN would be collected at a fixed time in relation to consumption of a standardized diet and meal size. However, Cai et al. (1994) report relatively stable PUN measured at 2-h intervals throughout the day in pigs with continuous free access to feed. If one needs to measure the parameters in a production setting on a large number of animals, it may not be feasible to standardize meal time, meal size, and time of blood sample collection; and the results of Cai et al. (1994) indicate it may not be necessary. Herein, blood samples were collected from animals in a common environment, including diet, which was available ad libitum. Time of blood sample collection in relation to feed consumption was not controlled.

Although it may not be necessary to be concerned about time of blood sampling relative to meal consumption in pigs with free access to feed, it may be important to consider the AA content of the diet the pigs are consuming. Examination of the results of Chen et al. (1995) yields evidence that relationship between nitrogen consumption and PUN values in gilts is cubic. Incremental changes in PUN due to increasing nitrogen consumption are least at low dietary CP, 10 to 13%, and high dietary CP, 19 to 25%. Plasma urea nitrogen concentrations are most responsive to changes in dietary nitrogen intake at CP levels near the recommended levels, between 13 and 19%. Genetic potential for protein accretion influenced the relationship between nitrogen intake and PUN values; however, the cubic relationship was preserved in both genetic lines examined. Subsequently, Chen et al. (1999) reported the effect of sex and dietary CP on PUN. The previously observed cubic relationship between dietary CP and PUN was seen in gilts, but the relationship was linear in barrows. These results reported by Chen et al. (1995, 1999) indicate that the pigs fed a diet formulated to approximately meet their requirement for AA (i.e., as per NRC recommendations) should segregate into more and less efficient utilizers of dietary AA based on PUN values.

Selection against high PUN, which would be selection for efficient use of dietary AA based upon the premise of the current study, should result in reduced nitrogen excretion, nitrogen concentration in manure, and ammonia entry into the atmosphere. The genetic correlations of PUN128 with BF21wk (0.87) and BW21wk (0.94) are strong and positive, suggesting that selection for lower PUN would have a favorable effect on fatness but an unfavorable effect on BW. The genetic correlations of PUN with rates of change in these traits were also high. The moderate to high phenotypic correlations between PUN and predicted adipose traits are expected. The urea in plasma arises from deamination of AA that are not used for body protein synthesis. The carbohydrate backbone of the deaminated AA is used for energy or synthesis of substances such as glucose, glycogen, or fatty acids that contribute to adipose accretion.

Ideally, selection against high PUN would result in pigs that have more desirable production traits (e.g., rates of BW and backfat gain, yield of marketable pork, and efficiency of feed use for production of marketable pork). However, reduced PUN and urea excretion alone may justify selection against high PUN. Improved use of dietary AA, and reduction in urea excretion and subsequent environmental impacts and costs associated with mitigation of excessive nitrogen in manure, may justify the selection efforts.

If PUN is an exploitable quantitative trait, then its use in selection of breeding animals may yield improvements in efficiency of dietary AA use and environmental impact. The overall mean PUN128 was 12.7 ± 5.4 mg/dL (mean ± SD) in boars, 16.6 ± 5.8 mg/dL in gilts, and 16.4 ± 6.4 mg/dL in barrows. If selection within boars and gilts was practiced to achieve 1 SD, the average selection differential would be 5.11 mg/dL. The genetic gain in reducing mPUN would be 1.1 mg/dL assuming heritability of 0.21. Assuming the castration effect would remain the same (+29%), mPUN in barrows would be about 15 mg/dL or 91% of the parental generation. These assumption-laden calculations suggest that genetic progress in reducing mPUN, and thus urinary excretion of urea, is possible.

IMPLICATIONS

Plasma urea nitrogen is influenced by sire line, sire, and sex and is heritable. Plasma urea may be an exploitable quantitative or additive trait that can be capitalized to improve efficiency of dietary protein use in, and reduce negative impacts of, pork production.

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